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GenCore version 5.1.3
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nucleic - nucleic search,	using sw model
Run on: February 16, 20	2003, 15:50:54 ; Search time 2481.53 Seconds (without alignments) 16465.781 Million cell updates/sec
Title: US-09-497-967-5 Perfect score: 1404 Sequence: 1 atgaagaacacatcctggt	tgatctcttactacctgc
Scoring table: IDENTITY_NUC Gapop 10.0 , Gap	
Searched: 2054640 seqs, 1	14551402878 residues
Total number of hits satisfying	chosen parameters: 4109280
Minimum DB seq length: 0 Maximum DB seq length: 200000000	
Post-processing: Minimum Match (Maximum Match) Listing first 4	0% 100% 45 summaries
Database : GenEmbl:* 1: 9b_ba:* 2: 9b_hig:* 4: 9b_on:* 5: 9b_pin:* 6: 9b_pat:* 7: 9b_pat:* 10: 9b_ro:* 10: 9b_ro:* 11: 9b_rs:* 12: 9b_ri:* 13: 9b_un:* 14: 9b_vi:* 15: em_ba:* 16: em_fun:* 17: em_hum:* 18: em_pi:* 20: em_ov:* 21: em_pi:* 22: em_ov:* 23: em_pi:* 24: em_pi:* 25: em_pi:* 26: em_to:* 27: em_pi:* 27: em_pi:* 28: em_hig-live:* 29: em_hig-live:* 30: em_hig-live:* 31: em_hig-live:* 32: em_hig-live:* 33: em_hig-live:* 34: em_hig-vrt:* 35: em_hig-vrt:* 36: em_higo_hum:* 37: em_higo_hum:* 38: em_higo_hum:* 41: em_higo_hum:* 42: em_higo_hum:* 36: em_higo_hum:* 40: em_higo_hum:* 40: em_higo_hum:* 40: em_higo_hum:* 40: em_higo_hum:*	* * * * * * * * * * * * * * * * * * *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8	귟	AF324424 Ichthyoph	AF140273 Ichthyoph	AF429315 Homo sap1	AF405431 Ichthyoph	M92907 Ichthyophth	ACOTAGO MIN MINES	ACOUNTY MUSCU	AF374493 Thalassio	Bos tau	rha.	AF374492 Thalassio	Sapter	HOMO S	Aycobac	4ycoba	sattu Sog t	AP005278 Corvoebac	equer	halas	AF374540 Thalassio	halas	halas	halas	halas	halaa	halas	halas	halassi	AF374491 Thalassio	halassi	halass	halas	AF37449/ Thalassio	halas halas	halas	halas	halassi	halassi	AF374504 Thalassio AF374505 Thalassio	Š			bp DNA linear INV 27-FEB-2002	T maketama				Oligohymenophorea;	X. Stieger K
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variation in primary sequence and tandem repeat i-antigens of Ichthyophthirius multifiliis Mol. Biochem. Parasitol. 120 (1), 93-106 (2002) 21839613
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Pred. No. 8.3e-218;
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2 (bases 1 to 3026)
2 Lin,Y., Lin,T.-L. and Clark,T.G.
Direct Submission
C Submitted (27-NOV-2000) Microbiology and University, Ithaca, NY 14883, USA
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Best Local Similarity 72.5%;
Matches 1013; Conservative
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Clark, T.G., Lin, T.-L., Jackwood, D.A. and Dickerson, H.W.
Direct Submission
Submitsed (29-MAR-1999) Microbiology & Immunology, Cornell
University, College of Veterinary Medicine, Ithaca, NY 14853, USA
                                                                                                                                                                                                                                The gene for an abundant parasite coat protein predicts tandemly repetitive metal binding domains Gene 229 (1-2), 91-100 (1999)
                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 2486)
Gaertig,J., Gao,Y., Tishgarten,T., Clark,T.G. and Dickerson,H.W.
Surface display of a parasite antigen in the ciliate Tetrahymena
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Ichthyophthirius multifiliis immobilization antigen precursor
                                                                                                                                 Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius:
1 (bases 1 to 2486)
Clark,T.G., Lin,T.L., Jackwood,D.A., Sherrill,J., Lin,Y. and
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    2486
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Pred. No. 5.6e-07;
0; Mismatches 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /isolate="G1"
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399. 1845
                                                                                            Ichthyophthirius multifillis. Ichthyophthirius multifillis
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/gene="IAG48"
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HGPEVLGYYTWBSGNTYQGTMAQGKRHGIGLESKGKWYYKGEWTHGFKGRYGVRECAG
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Holmes, S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L. Direct Submission
Submitted (05-00T-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                   Hwang, H.S.,
1218 TGCTGCTAACTTCTACACCACCAAGCAGACGGACTGGGTGGCTGGAATCGACACCTGTAC 1277
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Manmalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 125020)
Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H. Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A., A repeat expansion in the gene encoding junctophilin-3 is associated with Buntington disease-like 2
21583737
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                                                                     /map="16q24_3; between D16s520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
complement(35581. .35746)
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29056 a 32731 c 30696 g 28283 t
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/rpt_unit=ctg
complement(<36507. .>36887)
/gene="JPH3"
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/gene="JPH3"
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                                                                                                                                                                                                  CGTGATCCTGCAGACCGAGTGTCTGAACTGTGCTGCTAACTTCTACTTCGACGGAAACAA 1034
                         ATCGCARRKMMKSHAGRRRMCYYSKSWMSMBMSVSYSVKMHSMHASBSCMHWBKCMTWSC 16927
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199 ACCCCTTGICCTCAGAAGAAGGACGCTGGAGCTCAGCCTAACCCTCCTGCTACCGCTAAC
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TKCQANFYASKTSGFAAGTDTCTECSKKLTSGATAKVYAEATOKAQCASSTFAKFLSM
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Ichthyophthirius multifillis 52kDa immobilization antigen variant protein mRNA, complete cds.
AF405431
AF405431. GI:15290741
                                                                                                                                                                                                                      Variation in primary sequence and tandem repeat copy number among i-antiques of Ichthyophthirius multifillis
Mol. Biochem. Parasitol. 120 (1), 93-106 (2002)
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Ichthyophthirius multifillis.
Ichthyophthirius multifillis
Ebkaryopta, Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 1520)
Lin, Y., Lin, T.L., Wang, C.C., Wang, X., Stieger, K., Klopfleisch, R. and Clark, T.G.
Variation in primary sequence and tandem repeat copy number amony variation in primary sequence and tandem repeat copy number amony in-antigens of Ichthyophthirius multifilis
1 of Chilippophthirius multifilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Ichthyophthirius multifiliis"
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Lin,Y., Wang,J.C. and Clark,T.C.
Direct Submission
Submitted (03-AUG-2001) Microbiology of
University, Ithaca, NY 14853, USA
Location/Qualifiers
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/note="IAG52B[G5]"
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/isolate="G5"
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PAGTVLDDGTSTNFVASATECTKCSAGFFASKTTGFTAGTDTCTECTFKLTSGATAVN
                                     1249 bp mRNA linear INV 18-SEP-1998 multifiliis immobilization antigen precursor,
                                                                                                                                                                                                                                                                                                                 Clark, T.G., McGraw, R.A. and Dickerson, H.W.
Clark, T.G., McGraw, R.A. and Dickerson, H.W.
Developmental expression of surface antigen genes in the parasitic
clitate Ichthyophthirius multifillis
Proc. .Natl. Acad. Sci. U.S.A. 89 (14), 6363-6367 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-SEP-1998) Microbiology and Immunology, Cornell University, Ithaca, NY 14853, USA Sequence update by submitter on Sep 18, 1998 this sequence version replaced gi:159289.
                                                                                                                                ichthyophthirius multifillis.
Ichthyophthirius multifillis.
Eukaryota, Alveolata; Cillophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
I (bases 1 to 1249)
Lin, T.L. and Dickerson, H.W.
Purification and partial characterization of immobilization of J. Proctozool. 39 (4), 457-463 (1992)
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Submitted (06-JUN-1992) Microbiology and Immunology, Cornell
University, Ithaca, NY 14853, USA
4 (bases 1 to 1249)
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177. .893
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243 c 257 g
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                                                   Ichthyophthirius mult.
mRNA, partial cds.
M92907
M92907.1 GI:3628568
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'E 2 (bases 1 to 125020)

S Holmes, S.E. Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L.

Direct Submission

Direct Submission

L Submitted (05-0CT-2001) Psychiatry, Johns Hopkins Medical
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA

L. Caction/Qualifiers

I. 125020

/organism="Homo sapiens"

/db_xref="taxon:9606"
/chromosome="16"
/map="16q24.3; between D165520 and WI-12410"
/map="16q24.3; between D165520 and will Huntington's
Disease-Like 2 (HDL2)

eat_region complement(35581. .35746)
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HGFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Dutherita; Primates; Catarrhini; Hominidae; Homo.

( bases 1 to 125020]

Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S., Pingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A., Potter,N.T., Ross,C.A. and Margolis,R.L.
A repeat expansion in the gene encoding junctophilin-3 is Nat. Genet. 29 (4), 377-378 (2001)
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                                                                                               1098 TACCGCTGGAGGAACCGCTACCCTGATCGCTCAGTGTGCTCTGGAGTGTCCTGCTGGAAC 1157
                                                                                                                                1158 CGTGCTGACCGACGGAACCACCTCTACCTACAAGCAGGCTGCTTCTGAGTGTGAAGTG 1217
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       Score 52.2; DB 3;
Pred. No. 0.00089;
0; Mismatches 103;
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          3.78;
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Query Match 3.7 Best Local Similarity 52.5 Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGGGGSASRASCYKGRMSSKSCYRSGTRRRCMKSKCRRGSRGKSMGMTRGRSGGKTSYS 17136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17484 IGSYGSTGRSMKKKGYSKYSRGMKGKKKTCYCMWKYYKYRKTSMCWWYYMKSWGYKRYK 17425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCOMKKKGCTGYRGMSSKKSGYKSMRGMRGSSYSTSCWKSCWGYSWWKCMKYMSYKKKRR 17365
                                                                                                                                            17784 AGSKSSRGGTGTYMKKKGGKGSMSSKKWKGSSTSRRGSSAKSCSYMWGMSMCMSCMSM 17725
                                                                                                                                                                                                   17724 AKSYMMCYCYMYRMSSYMSYYKCYSCMGMSSTSYSYSCCWKMSSMGSCYKCMKYYSGWS 17665
                                                                                                                                                                                                                                                                  17664 SYSTSMGYYSSTSCKKYKCSWSSMYKCKTSKSYRRKRSYYWGGGRRAKKKYYCAGRRRR 17605
                                                                                                                                                                                                                                                                                                                          17544 YCMMRSSKSSSWSMSMSWCMGWGGGGRGRGRGGAGWRSSKGKRSTGMKRACSKK 17485
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                                                                                                                  274 AACGIGAAGIGICCIGCIGGAACCGCIAICGCIGGAGGAGCIACCGACIACGCIGCIAIC 333
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                                                                                                                                                                                334 ATCACCGAGTGTGAACTGTCGCATCAACTTCTACAACGAGAACGCTCCTAACTICAAC
                                                                                      17;
                                                         Length 125020;
              4254 others
                                                                                        Mismatches 406;
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0.0056;
              28283 t
NGAKYEGTWSNGLQDGYGTETYSDG"
1 32731 c 30696 g 28283
                                                          Score 50;
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                                                                                          93; Conservative 409;
                                                            3.6%;
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Best Local Similarity
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Consensus quality: 213156 bases at least Q40
Consensus quality: 22317 bases at least Q30
Consensus quality: 224719 bases at least Q30
Consensus quality: 224719 bases at least Q20
Estimated insert size: 258000; agarose-fp estimation
Estimated insert size: 228572 sum-of-contigs estimation
Guality coverage: 7.65 in Q20 bases; agarose-fp estimation
Quality coverage: 8.64 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence it currently
* NOTE: This is a 'working draft' sequence record is
* arbitrary. Gaps between the configs are represented as
* runs of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
AC073693 230372 bp DNA linear HTG 29-JUN-2000
MUS musculus clone RP23-152L22, WORKING DRAFT SEQUENCE, 19
                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                       Craniata; Vertebrata; Buteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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unknown length
of 18065 bp in length
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gap of unknown length
contig of 1528 bp in length
gap of unknown length
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of 8689 bp in length
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of 9596 bp in length
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unknown length
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of 5714 bp in length
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of 2215 bp in length
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Center clone name: RPCI-23_152L22
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Center: Joint Genome Institute
Center Code: JGI
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                Mammalia, Eutheria, Rodenti
1 (bases 1 to 230372)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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                                                                                                                 Mus musculus.
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Waterstow, Nation Department of Genetics, Washington Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Nov 17, 2001 this sequence version replaced gi:15887350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                        Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The clone sequenced to the left is RP11-549C16, 2000 bp overlap; the clone sequenced to the right is RP11-115D19. Actual start of this clone is at base position 123633 of RP11-549C16; actual end is at base position 159764 of RP11-582C12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong VECTOR: pBACCe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence derived from one plasmid subclone, base position 55515
                                            University School of Medicine, 4444 Forest Park Parkway, St. MO 53108, USA
6 ( bases 1 to 159764)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence of AC025608 has been incorporated into AC093866.
Location/Qualifiers
1. .159764
                                                                                                                                                                                                                                                                                           Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                         Center project name: H_NH0582C12
Drafting Center: WIBR
                                                                                                                                                                                                                                                                                                                                           ..... Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
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137. .299
/rpt_family="ERV1"
302. .653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP11-582C12"
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646. .735
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                                                                                                                                                                                                                                                                      Center code: WUGSC
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                                                                                                                                  TITLE
JOURNAL
                                                                                       REFERENCE
                                                                                                            AUTHORS
                                                                                                                                                                                                 COMMENT
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AC093866 AC025608
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Submitted (10-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Louis,
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1 (bases 1 to 159764).
Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 GCTGCTGTTTGGTGCCTGGAGCTTCTACCTGTACCCTTGTCCTCAGAAGAAGGACGCT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 GGAGCTCAGCCTAACCCTCCTGCTACCGCTAACCTGGTGACCCAGTGTAACGTGAAGTGT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Submitted (03-JAN-2002) Genome Sequencing Center, Washington
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98550 116262: contig of 17713 bpt in length 116263 116262: gap of unknown length 116363 116362: gap of unknown length 116363 140706: contig of 24344 bp in length 40807 140806: gap of unknown length 67609 167609: contig of 26603 bp in length 67610 167709: gap of unknown length 19399 19398: contig of 31689 bp in length 1939 230372: contig of 30874 bp in length Location/Qualifiers
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53740 c 52522 g 61042 t 1802 others
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Pearman, C., Meyer, R. and Doebber, A.
The sequence of Homo sapiens BAC clone RP11-582C12
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                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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3 (bases 1 to 159764)
Waterston, R.H.
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4 (bases 1 to 159764)
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3865. 3900
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12593. 12815
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Armbrust.B.V. and Galindo,H.M.
Rapid evolution of a sexual reproduction gene in centric diatoms of the genus Thalassiosira
Appl. Environ. Microbiol. 67 (8), 3501-3513 (2001)
21365169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           643 bp DNA linear PLN 27-JUL-2001
Thalassiosira weissflogii isolate CCMP 1336 clone 10 sexually
induced protein SIG 1 gene, partial cds.
AP374493
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Thalassiosira weissflogii
Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
Thalassiosirophycidae; Thalassiosirales; Thalassiosiraceae;
                                                                                                                                                                                                                                                                                                                                                                                              82 GAGACCAACACCGCTGGACAGGTGGACGACCTGGAACCCCTGCTAACTGTGTGAACTGT 141
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join(<1. 56,141. .>643)
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join(<1. 56,141. .>643)
/codon_start=2
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Best Local Similarity 52.69
Matches 90; Conservative
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1 (bases 1 to 179217)

8 Akhter.N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakseley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Lee-Lin,S.Q., Legaspl.R., Maduro,O.L., Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B., Mastrian,S.D., Portnoy,M.E., Frasad,A., Schueler,M.G., Stantripop,S., Thomas,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., NISC Comparative Sequencing Initiative

NISC Comparative Sequencing Initiative
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Bos taurus clone RP42-504H16, WORKING DRAFT SEQUENCE, 5 ordered
                                                                                                                                                                                                                                           278 TGAAGTGTCCTGCTGGAACCGCTATCGCTGGAGGAGCTACCGACTACGCTGCTATCATCA 337
                                                                                                                                                                                                                                                               338 CCGAGTGTGTGAACTGTCGCATCAACTTCTACAACGAAACGCTCCTAACTTCAAGGCTG 397
                                                                                                                                                                                                                                                                                                                                    Submitted (20-NOV-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 179217)
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Submitted (15-JUN-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Galthersburg, MD 20877, USA
On Jun 15, 2002 this sequence Version replaced gi:17017552.
                                                                                                                                                                                                                      ;
                                                                                                                                                                                 8; Length 643;
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/protein_id="AAK61135.1"
/db_xref="GI:14336350"
                                                                                                                                                                                                                  65; Indels
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                                                                                                                                                                             Score 41; DB 8
Pred. No. 1.6;
0; Mismatches
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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Matches 80; Conservative
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The sequence data in this record represents an 'enhanced' version of a phase 2 submission. Specifically, the indicated order and orientation of each sequence contigh has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in QSD bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 132314: contig of 32314 bp in length
                                                                                                                                                                                                                                                                                                                                       Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 177994 bases at least Q30
Consensus quality: 177894 bases at least Q30
Consensus quality: 178672 bases at least Q20
Insert size: 136000; agarose-fp
Insert size: 178817; sum-of-contigs
Quality coverage: 12.94x in Q20 bases; agarose-fp
Quality coverage: 9.85x in Q20 bases; sum-of-contigs
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/note="clone overlaps with GenBank Accession Number
AC113228 clone RP42-67B23 (center project name crl)"
1 38501 c 36655 g 49899 t 400 others
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66236: gap of unknown length
80633: contig of 14397 bp in length
80733: gap of unknown length
92700: contig of 11967 bp in length
92800: gap of unknown length
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Best Local Similarity 50.2%; Pred. No. 2.5;
Matches 101; Conservative 0; Mismatches 100; Indels
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/note="assembly_fragment"
66237. .80633
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/note="assembly_fragment"
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/db_xref="taxon:9913"
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vector_side:left"
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Center project name: crq Center clone name: 504H16

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/product="sexually induced protein SIG 1"
/protein_id="AAK70420.1"
/protein_id="AAK70420.1"
/dx xxef="dI:1458695"
/translation="SIDMCTCDRNFOGADCSLRTCPFGKAHVDTPRGDLDASLTIGDH
/translation="SIDMCTCDRNFOGADCSLRTCPFGKAHVDTPRGDLDASLTIGDH
NDIILAGSTLYPYGITEGFPLMSGTAGTVIANTAHDYMECSNKGLOPRINGLCECLPG
NDIILAGSTLYPYGITEGFPLMSGTAGTVIANTSAFHGRAAEVVORDGCSGHG
TCMTIEQLAFLDHGNTYDLWBCNYTMGCRCDPGYTGP"
1 146 g 149 t
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AF374552 1 GI:14586994
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Direct Submission
Submitted (27-ARR-2001) Oceanography, University of Washington, 357940, Seattle, WA 98195-7940, USA
Locattle, WA 98195-7940, USA
Location/Qualifiers
        Thalassiosira weissflogii.
Thalassiosira weissflogii
Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
Thalassiosirophycidae; Thalassiosirales; Thalassiosiraceae;
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                                                                                                                       963 AGCTACCAACTACGTGATCCTGCAGACCGAGTGTCTGAACTGTGCTGAACTTCTACTT 1022
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Appl. Environ. Microbiol. 67 (8), 3501-3513 (2001)
21365169
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Armbrust, E.V. and Galindo, H.M.
Rapid evolution of a sexual reproduction gene in
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/isolate="CCMP 1336"
/db_xref="taxon:67004"
/clone="13"
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Armbrust, E.V. and Galindo, H.M.
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Matches 79; Conservative
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AF374492 643 bp DNA linear PLN 27-JUL-2001
Thalassiosira weissflogii isolate CCMF 1336 clone 9 sexually
induced protein SIG 1 gene, partial cds.
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Armbrust, E.V. and Galindo, H.M.
Rapid evolution of a sexual reproduction gene in centric diatoms the genus Thalassiosira
Appl. Environ. Microbiol. 67 (8), 3501-3513 (2001)
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                                                                                                       Thalassiosira weissflogii.
Thalassiosira weissflogii
Eukaryota: stramenopiles; Bacillariophyta; Coscinodiscophyceae;
Thalassiosirophycidae; Thalassiosirales; Thalassiosiraceae;
Thalassiosira.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAACGCTCCTAACTTCAACGCTGGAGCTTCTACCTGTACCGCTTGTCC 422
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                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases I to 16814)
1 (bases I to 16814)
2 (ann. M. P., Pedeutour, F., Sirvent, N., Grosgeorge, J., Minoletti, F., Colndre, J.M., Terrier-Lacombe, M.J., Mandahl, N., Craver, R.D., Franssoon, I., Guilbaud, C. and Dumanski, J.P., Kedra, D., Franssoon, I., Guilbaud, C. and Dumanski, J.P., Mordanio of the platelet-derived growth factor B-chain gene via and glant-cell fibroblastoma and glant-cell fibroblastoma protuberans Nat. Genet. 15 (1), 95-98 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-JUN-1996) K.P. O'Brien, Dept. of Molecular Medicine, Clinical Genetics Unit, Karolinska Hospital, Building L-6, S-171 79 Stockholm, SwEDEN

Related Sequences: J03559, M10627, X07884, M20789 and K01228.

Location/Qualifiers

1. 16814

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REFERENCE
AUTHORS
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Kaneko,T., Nakamura,Y., Wolk,C.P., Kuritz,T., Sasamoto,S., Watanabe,A., Iriguchi,M., Ishikawa,A., Kawashima,K., Kimura,T., Kishida,Y., Kohara,M., Matsumoto,M., Matsuno,A., Muraki,A., Nakazaki,N., Shimpo,S., Sugimoto,M., Takazawa,M., Yamada,M., Yasuda,M., and Tabata,S.
                                                                                                                Nostoc sp. PCC 7120 plasmid pCC7120alpha DNA, complete genome, section 1/2.
AP003600.1 GI:17135539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-MAY-2001) Takakazu Kaneko, Kazusa DNA Research Submitted (02-MAY-2001) Takakazu Kaneko, Kazusa DNA Research; Yana 11stitute, The First Laboratory for Plant Gene Research; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:kaneko@kazusa.or.jp, VML:http://www.kazusa.or.jp/cyanobase/, Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                      Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120 DNA Res. 8 (5), 205-213 (2001) 2159288 2 (bases 1 to 341950)
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Kaneko, T.
Direct Submission
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46.7%; Pred. No. 11;
tive 0; Mismatches 139; Indels 0;
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tive 0; Mismatches 189; Indels
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Quality: Phrap Quality >=40 99.3% of Sequence:
Estimated Total Number of Errors is 0.9.
NOTE: This insert is not the entire sequence of the clone (entire
sequence is 232kb). It is clipped at the overlap with AC009002. The
number of bases overlapped is 5260.
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Homo sapiens chromosome 19 clone CTD-2639E6, complete sequence.
AC026803
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Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint
Schome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Genome Institute, 24271)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (16-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jul 16, 2002 this sequence version replaced gi:21637469.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission Submission Submission Submission Nation (01-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 22421) DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 224271)
DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                     326556 TGTCAAGGTGAGAGTGGTTTTATCGGTGGTAATTTGACTACCTGTGTTCAGGGTGACGGT 326497
Db 326616 GGTTATGGTGTGGTTAACTGCGTTAACGGTTATTGTTTGGGGAGTATTCCAGTTAGCGGA 326557
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                                                                   241 CCTCCTGCTACCGCTAACCTGGTGACCCAGTGTAACGTGAAGTGTCCTGCTGGAACCGCT 300
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Finishing Completed at Stanford Human Genome Center
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2.7%; Score 38.4; DB 9;
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/chromosome="19"
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